

OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/966,264

DATE: 10/16/2001

TIME: 15:04:40

Input Set : A:\Barber Sequence Listing.txt

Output Set: N:\CRF3\10162001\I966264.raw

3 <110> APPLICANT: Barber, Elizabeth K  
5 <120> TITLE OF INVENTION: Gene Expression Control Element DNA  
7 <130> FILE REFERENCE: 896034605001  
C--> 9 <140> CURRENT APPLICATION NUMBER: US/09/966,264  
C--> 9 <141> CURRENT FILING DATE: 2001-09-28  
9 <150> PRIOR APPLICATION NUMBER: US 60/237,079  
10 <151> PRIOR FILING DATE: 2000-09-30  
12 <160> NUMBER OF SEQ ID NOS: 33  
14 <170> SOFTWARE: PatentIn version 3.1  
16 <210> SEQ ID NO: 1  
17 <211> LENGTH: 137  
18 <212> TYPE: DNA  
19 <213> ORGANISM: human  
21 <220> FEATURE:  
22 <221> NAME/KEY: exon  
23 <222> LOCATION: (3)..(137)  
24 <223> OTHER INFORMATION:  
27 <220> FEATURE:  
28 <221> NAME/KEY: polyA\_site  
29 <222> LOCATION: (130)..(135)  
30 <223> OTHER INFORMATION:  
33 <400> SEQUENCE: 1  
34 at tat aaa gga aaa aga aaa taa cgc aat gga caa gtg gtg aag ctg 47  
35 Tyr Lys Gly Lys Arg Lys Arg Asn Gly Gln Val Val Lys Leu  
36 1 5 10  
38 tga act cag gtg tgc aca att atc agg aac acc cca aaa cca aag tga 95  
39 Thr Gln Val Cys Thr Ile Ile Arg Asn Thr Pro Lys Pro Lys  
40 15 20 25  
42 ggt aga aat agc atg aga agc cgt gtt tga tgt taa tta att 137  
43 Gly Arg Asn Ser Met Arg Ser Arg Val Cys Leu Ile  
44 30 35 40  
47 <210> SEQ ID NO: 2  
48 <211> LENGTH: 996  
49 <212> TYPE: DNA  
50 <213> ORGANISM: human  
52 <220> FEATURE:  
53 <221> NAME/KEY: exon  
54 <222> LOCATION: (1)..(996)  
55 <223> OTHER INFORMATION:  
58 <220> FEATURE:  
59 <221> NAME/KEY: misc\_feature  
60 <222> LOCATION: (710)..(996)  
61 <223> OTHER INFORMATION: Nucleotides 710-996 are homologous to a portion of human  
dystroph  
62 in DNA in the region of exon 79 except that nucleotides 860-996 a  
63 re inverted in comparison to the orientation of the same sequence  
64 in the dystrophin DNA  
67 <400> SEQUENCE: 2

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68	gtg gtt tga ttg ata gta aaa aaa atg ttc gtt aat aca agt aga gag	48
69	Val Val Leu Ile Val Lys Lys Met Phe Val Asn Thr Ser Arg Glu	
70	1 5 10 15	
72	taa gta atc aat caa tca ctc ata gcc aag gtg gaa aag atg tat ccc	96
73	Val Ile Asn Gln Ser Leu Ile Ala Lys Val Glu Lys Met Tyr Pro	
74	20 25 30	
76	atc atg gaa tat tcc tgt tct gat aga aat ctt gtg ctt atc tat gga	144
77	Ile Met Glu Tyr Ser Cys Ser Asp Arg Asn Leu Val Leu Ile Tyr Gly	
78	35 40 45	
80	att ctt ttg ata tat att tac att ggg aac ctg aat gta gct tga cat	192
81	Ile Leu Leu Ile Tyr Ile Tyr Ile Gly Asn Leu Asn Val Ala His	
82	50 55 60	
84	ttt tcc atg taa aca cca gta gcc tga tcc aac att aag ctg ata cta	240
85	Phe Ser Met Thr Pro Val Ala Ser Asn Ile Lys Leu Ile Leu	
86	65 70 75	
88	aca aac aac gtg taa tgg ctt cat taa taa ggc ttt gct tct tcc tgg	288
89	Thr Asn Asn Val Trp Leu His Gly Phe Ala Ser Ser Trp	
90	80 85	
92	aaa ctg gtg aaa aat caa acc ttg ttg tgt aca ccc tcg atg cag ctt	336
93	Lys Leu Val Lys Asn Gln Thr Leu Leu Cys Thr Pro Ser Met Gln Leu	
94	90 95 100	
96	ctg tgt tgt ctt cac cca gaa atg ggg aat gat ttc cca aat ggc aaa	384
97	Leu Cys Cys Leu His Pro Glu Met Gly Asn Asp Phe Pro Asn Gly Lys	
98	105 110 115 120	
100	gaa aca gag tga tgc tat cta tct gca cct ttt gta aag tct gtc ttt	432
101	Glu Thr Glu Cys Tyr Leu Ser Ala Pro Phe Val Lys Ser Val Phe	
102	125 130 135	
104	ctt tct ctt tgt ttt cca gga cac aat gta gga agt ctt ttc cac atg	480
105	Leu Ser Leu Cys Phe Pro Gly His Asn Val Gly Ser Leu Phe His Met	
106	140 145 150	
108	gca gat gat ttg ggc aga gcg atg gag tcc tta gta tca gtc atg aca	528
109	Ala Asp Asp Leu Gly Arg Ala Met Glu Ser Leu Val Ser Val Met Thr	
110	155 160 165	
112	gat gaa gaa gga gca gaa taa atg ttt tac aac tcc tga ttc ccg cat	576
113	Asp Glu Glu Gly Ala Glu Met Phe Tyr Asn Ser Phe Pro His	
114	170 175 180	
116	ggt ttt tat aat att cat aca aca aag agg att aga cag taa gag ttt	624
117	Gly Phe Tyr Asn Ile His Thr Thr Lys Arg Ile Arg Gln Glu Phe	
118	185 190 195	
120	aca aga aat aaa tct ata ttt ttg tga agg gta gtg gta tta tac tgt	672
121	Thr Arg Asn Lys Ser Ile Phe Leu Arg Val Val Val Leu Tyr Cys	
122	200 205 210	
124	aga ttt cag tag ttt cta agt ctg tta ttg ttt tgt taa caa tgg cag	720
125	Arg Phe Gln Phe Leu Ser Leu Leu Leu Phe Cys Gln Trp Gln	
126	215 220 225	
128	gtt tta cac gtc tat gca att gta caa aaa agt tat aag aaa act aca	768
129	Val Leu His Val Tyr Ala Ile Val Gln Lys Ser Tyr Lys Lys Thr Thr	
130	230 235 240	
132	tgt aaa atc ttg ata gct aaa taa ctt gcc att tct tta tat gga acg	816

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```

133 Cys Lys Ile Leu Ile Ala Lys      Leu Ala Ile Ser Leu Tyr Gly Thr
134                245                250                255
136 cat ttt ggg ttg ttt aaa aat tta taa cag tta taa aga aag aat tat      864
137 His Phe Gly Leu Phe Lys Asn Leu      Gln Leu      Arg Lys Asn Tyr
138                260                265                270
140 aaa gga aaa aga aaa taa cgc aat gga caa gtg gtg aag ctg tga act      912
141 Lys Gly Lys Arg Lys      Arg Asn Gly Gln Val Val Lys Leu      Thr
142                275                280
144 cag gtg tgc aca att atc agg aac acc cca aaa cca aag tga ggt aga      960
145 Gln Val Cys Thr Ile Ile Arg Asn Thr Pro Lys Pro Lys      Gly Arg
146 285                290                295
148 aat agc atg aga agc cgt gtt tga tgt taa tta att      996
149 Asn Ser Met Arg Ser Arg Val      Cys      Leu Ile
150 300                305
153 <210> SEQ ID NO: 3
154 <211> LENGTH: 13
155 <212> TYPE: PRT
156 <213> ORGANISM: human
158 <400> SEQUENCE: 3
160 Met Tyr Pro Ile Met Glu Tyr Ser Cys Ser Asp Arg Asn
161 1                5                10
164 <210> SEQ ID NO: 4
165 <211> LENGTH: 13
166 <212> TYPE: PRT
167 <213> ORGANISM: human
169 <400> SEQUENCE: 4
171 Tyr Ile Tyr Ile Gly Asn Leu Asn Val Ala Asp Thr Met
172 1                5                10
175 <210> SEQ ID NO: 5
176 <211> LENGTH: 18
177 <212> TYPE: PRT
178 <213> ORGANISM: human
180 <400> SEQUENCE: 5
182 Asp Asp Leu Gly Arg Ala Met Glu Ser Leu Val Ser Val Met Thr Asp
183 1                5                10                15
186 Glu Glu
190 <210> SEQ ID NO: 6
191 <211> LENGTH: 10
192 <212> TYPE: DNA
193 <213> ORGANISM: human
195 <400> SEQUENCE: 6
196 acttacctgt      10
199 <210> SEQ ID NO: 7
200 <211> LENGTH: 22
201 <212> TYPE: DNA
202 <213> ORGANISM: human
204 <400> SEQUENCE: 7
205 ttataaagaa agaattataa ag      22
208 <210> SEQ ID NO: 8

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209 <211> LENGTH: 42
210 <212> TYPE: DNA
211 <213> ORGANISM: human
213 <400> SEQUENCE: 8
214 ccttggctat gattgattga ttgattactt actctctact tg 42
217 <210> SEQ ID NO: 9
218 <211> LENGTH: 20
219 <212> TYPE: DNA
220 <213> ORGANISM: human
222 <400> SEQUENCE: 9
223 gattgatagt aaaaaaatg 20
226 <210> SEQ ID NO: 10
227 <211> LENGTH: 21
228 <212> TYPE: DNA
229 <213> ORGANISM: human
231 <400> SEQUENCE: 10
232 caatggcagg ttttacacgt c 21
235 <210> SEQ ID NO: 11
236 <211> LENGTH: 20
237 <212> TYPE: DNA
238 <213> ORGANISM: human
240 <400> SEQUENCE: 11
241 ggaaaagact tccacattgt 20
244 <210> SEQ ID NO: 12
245 <211> LENGTH: 22
246 <212> TYPE: DNA
247 <213> ORGANISM: human
249 <400> SEQUENCE: 12
250 ctttttcctt tataattctt tc 22
253 <210> SEQ ID NO: 13
254 <211> LENGTH: 22
255 <212> TYPE: DNA
256 <213> ORGANISM: human
258 <400> SEQUENCE: 13
259 catcaaacac ggcttctcat gc 22
262 <210> SEQ ID NO: 14
263 <211> LENGTH: 9
264 <212> TYPE: PRT
265 <213> ORGANISM: human
267 <220> FEATURE:
268 <221> NAME/KEY: MISC_FEATURE
269 <222> LOCATION: (1)..(3)
270 <223> OTHER INFORMATION: histone methylation site
273 <220> FEATURE:
274 <221> NAME/KEY: MISC_FEATURE
275 <222> LOCATION: (7)..(9)
276 <223> OTHER INFORMATION: histone methylation site
279 <400> SEQUENCE: 14
281 Arg Lys Asn Tyr Lys Gly Lys Arg Lys

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282 1          5
285 <210> SEQ ID NO: 15
286 <211> LENGTH: 18
287 <212> TYPE: DNA
288 <213> ORGANISM: human
290 <400> SEQUENCE: 15
291 gttcgttaat acaagtag                      18
294 <210> SEQ ID NO: 16
295 <211> LENGTH: 18
296 <212> TYPE: DNA
297 <213> ORGANISM: human
299 <400> SEQUENCE: 16
300 gccaaaggtgg aaaagatg                      18
303 <210> SEQ ID NO: 17
304 <211> LENGTH: 18
305 <212> TYPE: DNA
306 <213> ORGANISM: human
308 <400> SEQUENCE: 17
309 ccagtagcct gatccaac                      18
312 <210> SEQ ID NO: 18
313 <211> LENGTH: 15
314 <212> TYPE: DNA
315 <213> ORGANISM: human
317 <400> SEQUENCE: 18
318 ggcttcatta ataag                        15
321 <210> SEQ ID NO: 19
322 <211> LENGTH: 17
323 <212> TYPE: DNA
324 <213> ORGANISM: human
326 <400> SEQUENCE: 19
327 ggcaaagaaa cagagtg                      17
330 <210> SEQ ID NO: 20
331 <211> LENGTH: 17
332 <212> TYPE: DNA
333 <213> ORGANISM: human
335 <400> SEQUENCE: 20
336 caggacacaa tgtagga                      17
339 <210> SEQ ID NO: 21
340 <211> LENGTH: 23
341 <212> TYPE: DNA
342 <213> ORGANISM: human
344 <400> SEQUENCE: 21
345 gttataaaga aagaattata aag                23
348 <210> SEQ ID NO: 22
349 <211> LENGTH: 18
350 <212> TYPE: DNA
351 <213> ORGANISM: human
353 <400> SEQUENCE: 22
354 gaaaataacg caatggac                      18

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/966,264

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Input Set : A:\Barber Sequence Listing.txt

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L:9 M:270 C: Current Application Number differs, Replaced Current Application No

L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date